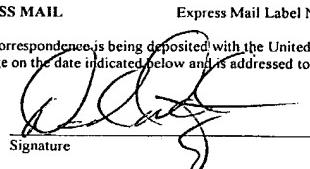


SUBSTITUTE FORM PTO-1390 U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER 06501-085001	
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371		U.S. APPLICATION NO. (If Known, see 37 CFR 1.5) 09/937162	
INTERNATIONAL APPLICATION NO. PCT/JP00/01778	INTERNATIONAL FILING DATE 23 March 2000	PRIORITY DATE CLAIMED 23 March 1999	
TITLE OF INVENTION METHOD FOR SCREENING ANTICANCER AGENT APPLICANT(S) FOR DO/EO/US Yoshihiro Sowa and Tetsuro Orita			
<p>Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:</p> <ol style="list-style-type: none"> 1. <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371. 2. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371. 3. <input checked="" type="checkbox"/> This is an express request to promptly begin national examination procedures (35 U.S.C. 371(f)). 4. <input checked="" type="checkbox"/> The US has been elected by the expiration of 19 months from the priority date (PCT Article 31). 5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2)) <ol style="list-style-type: none"> a. <input type="checkbox"/> is attached hereto (required only if not communicated by the International Bureau). b. <input checked="" type="checkbox"/> has been communicated by the International Bureau. c. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). 6. <input checked="" type="checkbox"/> An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)). 7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)) <ol style="list-style-type: none"> a. <input type="checkbox"/> are attached hereto (required only if not communicated by the International Bureau). b. <input type="checkbox"/> have been communicated by the International Bureau. c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. d. <input checked="" type="checkbox"/> have not been made and will not be made. 8. <input type="checkbox"/> An English language translation of amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)). 9. <input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). 10. <input type="checkbox"/> An English language translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)). <p>Items 11 to 16 below concern other documents or information included:</p> <ol style="list-style-type: none"> 11. <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98. 12. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included. 13. <input checked="" type="checkbox"/> A FIRST preliminary amendment. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment. 14. <input type="checkbox"/> A substitute specification. 15. <input type="checkbox"/> A change of power of attorney and/or address letter. 16. <input checked="" type="checkbox"/> Other items or information: <ul style="list-style-type: none"> <input checked="" type="checkbox"/> Informal Sequence Listing, 9 pages <input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> 			
CERTIFICATE OF MAILING BY EXPRESS MAIL		Express Mail Label No E624321195US <small>I hereby certify under 37 CFR §1.10 that this correspondence is being deposited with the United States Postal Service as Express Mail Post Office to Addressee with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.</small>	
<small>September 21, 2001</small> <small>Date of Deposit</small>		 <small>Derek Doherty</small> <small>Typed Name of Person Signing</small>	

U.S. APPLICATION NO. (IF KNOWN) 09/937162	INTERNATIONAL APPLICATION NO. PCT/JP00/01778	ATTORNEY'S DOCKET NUMBER 06501-085001
17. <input checked="" type="checkbox"/> The following fees are submitted:		CALCULATIONS PTO USE ONLY
Basic National Fee (37 CFR 1.492(a)(1)- (5)):		
Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO..... \$1000		
International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$860		
International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$710		
International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4) \$690		
International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4) \$100		
ENTER APPROPRIATE BASIC FEE AMOUNT =		
		\$860.00
Surcharge of \$130 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).		\$0.00
Claims	Number Filed	Number Extra
Total Claims	19 - 20 =	0
Independent Claims	2 - 3 =	0
MULTIPLE DEPENDENT CLAIMS(S) (if applicable)		+ \$270
TOTAL OF ABOVE CALCULATIONS =		
		\$860.00
<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.		\$0.00
SUBTOTAL =		
Processing fee of \$130 for furnishing the English Translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f))		\$0.00
TOTAL NATIONAL FEE =		
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property +		\$0.00
TOTAL FEES ENCLOSED =		
		Amount to be refunded:
		Charged:
a. <input checked="" type="checkbox"/> A check in the amount of \$860.00 to cover the above fees is enclosed.		
b. <input type="checkbox"/> Please charge my Deposit Account No. 06-1050 in the amount of \$0.00 to cover the above fees. A duplicate copy of this sheet is enclosed.		
c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 06-1050. A duplicate copy of this sheet is enclosed.		
NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b) must be filed and granted to restore the application to pending status.		
SEND ALL CORRESPONDENCE TO:		
Janis K. Fraser, Ph.D., J.D. FISH & RICHARDSON P.C. 225 Franklin Street Boston, Massachusetts 02110-2804 (617) 542-5070 phone (617) 542-8906 facsimile		
 SIGNATURE: NAME _____ REGISTRATION NUMBER _____ 34,819		Janis K. Fraser, Ph.D., J.D.

PTO/PCT RECEIVED 30 OCT 2002

Attorney's Docket No.: 06501-085001 / C2-101PCT-US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Yoshihiro Sowa et al.
Serial No. : 09/937,162
Filed : September 21, 2001
Title : METHOD FOR SCREENING ANTICANCER AGENT

BOX PCT

Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

In response to the communication dated August 30, 2002 (copy enclosed), applicants submit herewith a Sequence Listing in computer-readable form as required by 37 CFR §1.824. In addition, applicants submit a substitute Sequence Listing as required under 37 CFR §1.823(a) and a statement under 37 CFR §1.821(f).

Applicants respectfully request entry of the paper copy and computer-readable copy of the Sequence Listing filed herewith for the instant application. Furthermore, applicants request entry of the following amendments.

In the specification:

Replace the original Sequence Listing with the substitute Sequence Listing filed herewith.

Replace the paragraph beginning at page 8, line 6, with the following rewritten paragraph:

--The binding sequence of the heteroprotein used for the construction of the second vector of this invention is not specially limited as long as the fusion protein expressed by the first expression vector can bind specifically to the binding sequence. For example, if the fusion protein comprises the GAL4 DNA binding region, the binding sequence can be, for example, "5'-cggasgacwgtcstccg-3' (SEQ ID NO:19); s= c or g, w= a or t" (Marmorstein, R. et al., 1992, Nature 356: 408-414). If the fusion protein comprises the LexA DNA binding region, the

CERTIFICATE OF MAILING BY EXPRESS MAIL

Express Mail Label No. EL932143291US

October 30, 2002

Date of Deposit

Applicant : Yoshihiro Sowa et al.
Serial No. : 09/937,162
Filed : September 21, 2001
Page : 2

Attorney's Docket No.: 06501-085001 / C2-101PCT-
US

binding sequence can be, for example, "5'-ctgttnnnnnnnacag-3' (SEQ ID NO:20); n= a, t, g, or c" (Erica, A. et al., 1992, Mol. Cell. Biol., 12: 3006-3014). If the fusion protein comprises the DNA binding domain of tetracycline repressor protein (Tet R), the binding sequence can be, for example, "5'-tccctatcagtgatagaga-3'" (SEQ ID NO:21) (Manfred, G. et al., 1992, Proc. Natl. Acad. Sci. USA, 89: 5547-5551).--

Applicant : Yoshihiro Sowa et al.
Serial No. : 09/937,162
Filed : September 21, 2001
Page : 3

Attorney's Docket No.: 06501-085001 / C2-101PCT-US

REMARKS

Applicants hereby submit that the enclosures fulfill the requirements under 37 C.F.R. §1.821-1.825. The amendments in the specification merely insert sequence identifiers in the specification and replace the original Sequence Listing with an amended substitute Sequence Listing. The substitute Sequence Listing contains the nucleic acid sequences disclosed at page 8 of the specification. No new matter has been added.

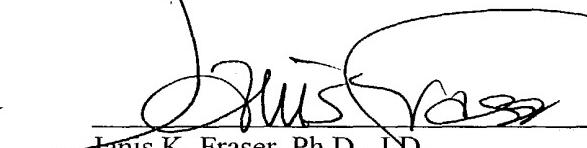
Attached hereto is a marked-up version of the changes made to the specification by the current amendment.

Please apply any charges or credits to Deposit Account No. 06-1050, referencing attorney docket number 06501-085001.

Respectfully submitted,

Date:

Oct. 30, 2002


Janis K. Fraser, Ph.D., J.D.
Reg. No. 34,819

Fish & Richardson P.C.
225 Franklin Street
Boston, Massachusetts 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

Applicant : Yoshihiro Sowa et al.
Serial No. : 09/937,162
Filed : September 21, 2001
Page : 4

Attorney's Docket No.: 06501-085001 / C2-101PCT-US

"Version With Markings to Show Changes Made"

In the specification:

Paragraph beginning at page 8, line 6, has been amended as follows:

The binding sequence of the heteroprotein used for the construction of the second vector of this invention is not specially limited as long as the fusion protein expressed by the first expression vector can bind specifically to the binding sequence. For example, if the fusion protein comprises the GAL4 DNA binding region, the binding sequence can be, for example, "5'-cggasgacwgtcstccg-3' (SEQ ID NO:19); s= c or g, w= a or t" (Marmorstein, R. et al., 1992, Nature 356: 408-414). If the fusion protein comprises the LexA DNA binding region, the binding sequence can be, for example, "5'-ctgtnnnnnnnnacag-3' (SEQ ID NO:20); n= a, t, g, or c" (Erica, A. et al., 1992, Mol. Cell. Biol., 12: 3006-3014). If the fusion protein comprises the DNA binding domain of tetracycline repressor protein (Tet R), the binding sequence can be, for example, "5'-tccctatcagtgatagaga-3'" (SEQ ID NO:21) (Manfred, G. et al., 1992, Proc. Natl. Acad. Sci. USA, 89: 5547-5551).

09/937162

JC16 Rec'd PCT/PTO SEP 21 2001
Attorney's Docket No.: 06501-085001/C2-101PCT-US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Yoshihiro Sowa et al. Art Unit : Unknown
Serial No. : Examiner : Unknown
Filed : Herewith
Title : METHOD FOR SCREENING ANTICANCER AGENT

Box PCT

Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Prior to examination, please amend the application as follows:

In the claims:

Cancel claims 1 to 5.

Add claims 6 to 24.

-- 6. A method of identifying an agent having cellular anti-proliferation activity, comprising:

providing a cell having (a) a first vector comprising a first regulatory sequence operably linked to a nucleic acid sequence encoding a fusion protein, wherein the fusion protein comprises (i) Sp3 or a fragment thereof having transcriptional activation activity and (ii) a DNA binding domain of a heterologous protein; and (b) a second vector comprising a target binding sequence for the DNA binding domain of the fusion protein operably linked to a reporter gene;

contacting the cell with a test agent; and

selecting a test agent that increases the expression of the reporter gene compared to a control.

CERTIFICATE OF MAILING BY EXPRESS MAIL

Express Mail Label No. EL624321195US

I hereby certify under 37 CFR §1.10 that this correspondence is being deposited with the United States Postal Service as Express Mail Post Office to Addressee with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

Date of Deposit

September 21, 2001

Signature

DEVER D'HERITY
Typed or Printed Name of Person Signing Certificate

Applicant : Yoshihiro Sowa et al.
Serial No. :
Filed : Herewith
Page : 2

Attorney's Docket No.: 06501-085001

7. The method of claim 6, wherein the heterologous protein is not endogenous to the cell.

8. The method of claim 7, wherein the heterologous protein is GAL4, LexA or tetracycline repressor.

9. The method of claim 6, wherein the reporter gene encodes luciferase, chloramphenicol acetyltransferase, beta-galactosidase, human growth hormone or secreted alkaline phosphatase.

10. The method of claim 8, wherein the reporter gene encodes luciferase, chloramphenicol acetyltransferase, beta-galactosidase, human growth hormone or secreted alkaline phosphatase.

11. The method of claim 6, wherein the fusion protein comprises at least one glutamine-rich region of Sp3.

12. The method of claim 8, wherein the fusion protein comprises at least one glutamine-rich region of Sp3.

13. The method of claim 9, wherein the fusion protein comprises at least one glutamine-rich region of Sp3.

14. The method of claim 6, wherein the second vector comprises a second regulatory sequence operably linked to the reporter gene.

15. The method of claim 8, wherein the second vector comprises a second regulatory sequence operably linked to the reporter gene.

Applicant : Yoshihiro Sowa et al.
Serial No. :
Filed : Herewith
Page : 3

Attorney's Docket No.: 06501-085001

16. The method of claim 9, wherein the second vector comprises a second regulatory sequence operably linked to the reporter gene.

17. The method of claim 6, wherein the test agent is a low molecular weight compound.

18. The method of claim 6, further comprising evaluating the selected test agent for anti-cancer activity.

19. The method of claim 18, wherein the test agent is evaluated for anti-cancer activity *in vitro*.

20. The method of claim 18, wherein the test agent is evaluated for anti-cancer activity *in vivo*.

21. An anticancer agent comprising a compound that increases the transcriptional activity mediated by Sp3 and a pharmaceutical carrier, wherein the anticancer agent is not TSA, trapoxin, or sodium butyrate.

22. An anticancer agent identified by the method of claim 6, wherein the anticancer agent is not TSA, trapoxin, or sodium butyrate.

23. An anticancer agent identified by the method of claim 8, wherein the anticancer agent is not TSA, trapoxin, or sodium butyrate.

24. An anticancer agent identified by the method of claim 9, wherein the anticancer agent is not TSA, trapoxin, or sodium butyrate--

Applicant : Yoshihiro Sowa et al.
Serial No. :
Filed : Herewith
Page : 4

Attorney's Docket No.: 06501-085001

REMARKS

Claims 6 to 24 are pending in this application, claims 1 to 5 having been cancelled by the above amendment and new claims 6 to 24 added. New claims 6 to 24 are supported by original claims 1-5 and by the specification, e.g., at page 7, lines 9-14; page 9, lines 19-25; and page 10, lines 8-11. No new matter has been added.

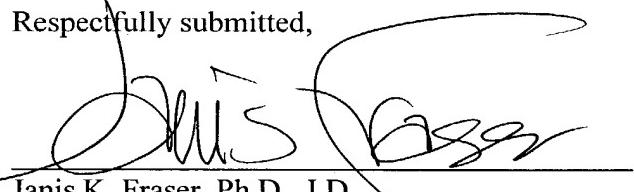
Attached is a marked-up version of the changes being made by the current amendment.

Please apply any other charges or credits to Deposit Account No. 06-1050.

Date:

Sept. 21, 2001

Respectfully submitted,


Janis K. Fraser, Ph.D., J.D.
Reg. No. 34,819

Fish & Richardson P.C.
225 Franklin Street
Boston, Massachusetts 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

Applicant : Yoshihiro Sowa et al.
Serial No. :
Filed : Herewith
Page : 5

Attorney's Docket No.: 06501-085001

Version with markings to show changes made

In the claims:

Cancel claims 1 to 5.

SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

<120> Methods for screening anti-tumor agents

<130> C2-101PCT

<140>

<141>

<150> JP 1999-77350

<151> 1999-03-23

<160> 18

<170> PatentIn Ver. 2.0

<210> 1

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized oligonucleotide sequence

<400> 1

cgggtccgc ctcctt

16

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized oligonucleotide sequence

<400> 2

agctcgggtc ccgcctcctt

20

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized oligonucleotide sequence

<400> 3

tcgaaaggag gcgggacccg

20

<210> 4

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 4

acaggtgagc ttga

14

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 5

tcagaagcca ttgcc

15

4/9

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 6

ccaaaaaaga agagaaaaggtaaccggcg 30

<210> 7

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 7

gaagcatgca cctgc 15

<210> 8

<211> 23

<212> DNA

<213> Artificial Sequence

220

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 8

cggatccat tccaaatgtct gct

23

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

220

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 9

ataggatcct tactccattg tctcatttcc

30

〈210〉 10

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 10

cgggatccaa ctctatagat tctgct

26

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 11

gcggatccca ctgttaactgt ttgttag

26

<210> 12

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 12

cgggatccgg ctctaatcaa accttact

28

<210> 13

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 13

cgggatccgg cattaatgcc gacggaca

28

<210> 14

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 14

cgggatccca gggaaattat atccagtc

28

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially
synthesized primer sequence

<400> 15

cgggatccag gaatgatctg aatttgac

28

<210> 16

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially
synthesized primer sequence

<400> 16

cgggatccctg cagtcattgt ctgagaac

28

<210> 17

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 17

cgggatccaa gatctgaaga atgaacct

28

<210> 18

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an artificially synthesized primer sequence

<400> 18

cgggatccaa aggttccagg attcagct

28

Li / Prys

METHOD FOR SCREENING ANTICANCER AGENT

5

Technical Field

The present invention relates to a method for screening an anticancer agent. It specifically relates to a method for screening an anticancer agent targeting the Sp3 protein involved in the tumor-suppressing mechanism.

10

Background Art

Cancer is caused by a series of genetic alterations destroying the normal mechanisms that control the cell cycle, differentiation, and morphology. A large number of natural compounds have been isolated based on their ability to restore cells having abnormal morphology, to induce cell differentiation, and to stop uncontrolled cell cycles in various cancer cells and transformed cells. Trichostatin A (TSA) (Sugita K et al. (1992). Cancer Res., 52, 168-172) and trapoxin (Itazaki H et al. (1990). J. Antibiot., 43, 1524-1532) have been isolated as substances capable of suppressing transformation. These substances also induce cell differentiation and cell cycle arrest. However, it was not clear how these materials showed such tumor-suppressing activity.

20

It is the current belief that histone deacetylases (HDAC) are the target of these drugs. Actually, TSA and trapoxin inhibit HDAC activity at the same concentration in which they show antitumor activity (Yoshida et al., 1990, J. Biol. Chem., 265:17174-17179; Kijima M et al., 1993 J. Biol. Chem., 268, 22429-22435). Rapidly accumulating findings suggest that acetylation and deacetylation of histone and non-histone proteins

25

play an important role in the transcriptional control of eukaryotic cells (Wolffe AP and Pruss D. (1996). Cell, 84, 817-819; Wade PA et al. (1997). TIBS, 22, 128-132; Pazin MJ and Kadonaga JT. (1997). Cell, 89, 325-328; Struhl K. (1998). Genes Dev., 12, 599-606; Kuo MH and Allis CD. (1998). Bioessays, 20, 615-626). Since many transcription factors, transcription coactivators, and basic transcription initiation complex proteins

30

have histone acetyltransferase activity, it became clear that acetylation of histone plays an important role in the initiation and promotion of transcription. Furthermore, the recent

cloning of some of the HDACs, and the fact transcriptional repressors, and transcription corepressors form complexes with HDAC, gradually revealed that HDAC plays an important role in transcriptional repression (Wolffe AP. (1997). Nature, 387, 16-17). As HDAC inhibitors show antitumor activity, HDAC may repress transcription of a group of 5 antitumor genes whose products induce cell proliferation arrest or cell differentiation (DePinho RA. (1998). Nature, 391, 533-536).

The present inventors earlier proved that sodium butyrate, which is well known as a differentiation inducer and acts as a HDAC inhibitor at micro molar concentrations, induced the expression of p21/WAF1/Cip1, which is a cyclin-CDK inhibitor (a negative 10 regulator of cell cycle) acting independently of p53 (Nakano K et al. (1997). J. Biol. Chem., 272, 22199-22206). They also reported that both sodium butyrate and TSA activated p21/WAF1/Cip1 gene promoter through the Sp1 binding sequence (Sowa Y et al. (1997). Biochem. Biophys. Res. Comm., 241, 142-150). Interestingly, it was reported 15 recently that the Sp1 binding site in p21/WAF1/Cip1 promoter was also involved in the induction of p21/WAF1/Cip1 by TGF- β , phorbol ester, okadaic acid, progesterone, or geranylgeranyl-transferase I inhibitor GGTI-298 (Datto MB et al. (1995). J. Biol. Chem., 270, 28623-28628; Biggs JR et al. (1996). J. Biol. Chem., 271, 901-906; Adnane J et al. (1998). Mol. Cell. Biol., 18, 6962-6970; Owen GI et al. (1998). J. Biol. Chem., 273, 20 10696-10701). Among these, TGF- β and GGTI-298 have been reported to induce transcription of p21/WAF1/Cip1 by enhancing the transcriptional activity of Sp1, whereas progesterone accomplishes the same through Sp1 and CBP/p300 (Li JM et al. (1998). Nucleic Acids Res., 26, 2449-2456; Owen GI et al. (1998). J. Biol. Chem., 273, 10696-10701).

These reports are thought to suggest the induction of transcription by SP1-mediated activation of histone acetyltransferase. Histone acetylation is thought to be 25 involved in the transcriptional activation of many genes. In contrast, histone deacetylation is considered to be involved in transcriptional repression, although the detailed mechanism is not clear. Recently, it was reported that transcriptional repressors N-CoR and SMRT repressed the transcription specific to a DNA sequence by binding to 30 intranuclear transcription factors (Horlein AJ et al. (1995). Nature, 377, 397-404; Kurokawa R et al. (1995). Nature, 377, 451-454; Chen JD and Evans RM. (1995).

Nature, 377, 454-457). As these factors bind to HDAC simultaneously and form a higher order complex, it is suggested that the rigid organization of chromatin, which is mediated by histone deacetylation, represses transcription (Pazin MJ and Kadonaga JT. (1997). Cell, 89, 325-328; Heinzel T et al. (1997). Nature, 387, 43-48; Allard L et al. (1997) 5 Nature, 387, 49-55). In fact, studies using a fusion protein of promyelocytic leukemia or promyelocytic leukemia zinc-finger protein and retinoic acid receptor revealed that the binding of HDAC was necessary for transcriptional repression (Lin RJ et al. (1998). Nature, 391, 811-814; Grignani F et al. (1998). Nature, 391, 815-818; He LZ et al. (1998). Nature Genet., 18, 126-135). A similar HDAC-mediated mechanism of 10 transcriptional repression specific to a DNA sequence was revealed also in the case of Myc/Mad/Max (Hassig C et al. (1997). Cell, 89, 341-347; Laherty CD et al. (1997). Cell, 89, 349-356), E2F/Rb (Brehm A et al. (1998). Nature, 391, 597-601; Magnaghi-Jaulin L et al. (1998). Nature, 391, 601-605; Luo RX et al. (1998). Cell, 92, 463-473), and in the case of DNA methylation (Nan X et al. (1998). Nature, 393, 386-389; Jones PL et al. 15 (1998). Nature Genet., 19, 187-191). However, it was not clear whether or not a specific transcription factor capable of binding to the Sp1 binding sequence mediates the transcriptional activation signal by a HDAC inhibitor.

Disclosure of the Invention

20 An objective of this invention is to provide an efficient method for screening an anticancer agent.

The present inventors reported that TSA, which is known to be a HDAC inhibitor having a tumor-suppressing effect, activated the p21/WAF1/Cip1 promoter through the Sp1 binding sequence (Nakano K et al. (1997). J. Biol. Chem., 272, 22199-22206; Sowa 25 et al. (1997). Biochem, Biophys. Res. Comm., 241, 142-150). The inventors thought it might be possible to screen an anticancer agent targeting a novel molecule by identifying a new molecule involved in the signal transduction leading to the activation of the p21/WAF1/Cip1 promoter in response to a TSA stimulus.

Therefore, using gel mobility shift assays of the MG63 cell nuclear extract, the 30 inventors first searched for factors that bound to the Sp1 binding sequence in the p21/WAF1/Cip1 promoter during the activation of the promoter by TSA. Thereby, they

revealed that Sp1 and Sp3 were the main molecules that bound to the Sp1 binding sequence in the p21/WAF1/Cip1 promoter (Lania L et al. (1997). Int. J. Biochem. Cell Biol., 29, 1313-1323).

In addition to the p21/WAF1/Cip1 promoter, the inventors also examined the function of Sp1 and Sp3 by an assay system using the luciferase gene, which is activated depending on the GAL4 binding sequence, as the reporter gene. They revealed that transcriptional induction of the reporter gene by TSA occurred in the presence of GAL4-Sp3, which is a fusion protein of GAL4 and Sp3, but it did not occur in the presence of GAL4-Sp1, which is a fusion protein of GAL4 and Sp1. Furthermore, by constructing various Sp3 deletion mutants, they showed that transcriptional activation in response to a TSA stimulus could occur if at least one of the two glutamine-rich domains contained in the transcription activation domain was present. They also revealed that the forced expression of dominant negative Sp3 that lacks a transcription activation domain repressed the TSA-mediated activation of p21/WAF1/Cip1 promoter and that of the promoter activated through the Sp1 binding sequence.

These results prove that Sp3 is involved in the transcriptional activation of p21/WAF1/Cip1 by TSA. These results also suggest that the screening of anticancer agents targeting Sp3 might be possible. The assay system developed by the inventors using the luciferase gene activated depending on the GAL4 sequence as the reporter gene, is especially appropriate for efficiently screening anticancer agents.

This invention relates to a method for screening an anticancer agent targeting the Sp3 protein involved in tumor suppression. It especially relates to a method for efficiently screening an anticancer agent using the luciferase gene activated depending on the GAL4 binding sequence as the reporter gene. This invention specifically relates to:

- 25 (1) a method for screening an anticancer agent comprising the steps of:
 - (a) preparing a cell carrying (i) a first vector comprising, in an expressible manner, DNA encoding a fusion protein comprising a region having the transcriptional activation capacity of the Sp3 protein and a region having the DNA binding capacity of a heteroprotein, and ,(ii) a second vector comprising a binding sequence of the
 - 30 heteroprotein, an expression regulatory sequence activated by the binding of the fusion protein, and a downstream reporter gene functionally bound to the regulatory sequence,

- 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13
- (b) contacting a test sample with the cell and measuring reporter activity, and,
(c) selecting a compound that elevates reporter activity in comparison with a control test in which the test sample is not contacted with the cell,
- (2) the method of (1), wherein the heteroprotein is the GAL4 protein, LexA protein, or tetracycline repressor protein,
- 5 (3) the method of (1) or (2), wherein the reporter gene is encoding luciferase, chloramphenicol acetyltransferase, beta-galactosidase, human growth hormone, or secreted alkaline phosphatase,
- (4) an anticancer agent comprising a compound that enhances Sp3-mediated transcriptional activity as an active ingredient, and,
- 10 (5) the anticancer agent of (4), wherein the agent can be isolated by a method of any one of (1) to (3).

As shown in the Examples, the transcription activation domain of Sp3 can elevate the transcription from p21/WAF1/Cip1 promoter. p21/WAF1/Cip1 gene has a cell proliferation suppressing effect, and its expression is elevated by TSA known to have a tumor-suppressing effect. The expression of p21/WAF1/Cip1 is also known to be induced through the Sp1 binding sequence by plural HDAC inhibitors closely related to antitumor effects. As this invention revealed that Sp3 was involved in the induction of transcription through the Sp1 binding sequence, it is thought that the treatment and prevention of cancer are also possible by enhancing the activity of Sp3 that suppresses cell neoplasia.

The method of this invention for screening an anticancer agent is based on the finding by the inventors that Sp3 is involved in the signal transduction leading to the expression of antitumor effects in response to a TSA stimulus. This method is also based on the finding that the system developed by the inventors for detecting the transcriptional activity of Sp3 using a reporter gene can also be used for the screening of a compound that has an antitumor effect similar to TSA.

The principle behind the screening method of this invention is as follows: First, the vectors are constructed. The first vector comprises, in an expressible manner, DNA encoding a fusion protein comprising a region having the transcriptional activation capacity of the Sp3 protein and a region having the DNA binding capacity of a

heteroprotein. The second vector comprises the binding sequence of the heteroprotein, an expression regulatory sequence activated by the binding of the fusion protein, and a downstream reporter gene functionally bound to the regulatory sequence. These vectors are then introduced into a cell. In this cell, the fusion protein that comprises the region
5 having transcriptional activation capacity of Sp3 protein and the region having DNA binding capacity of the heteroprotein is expressed through the first vector. The fusion protein binds to the expression regulatory region in the second vector through the DNA binding region derived from the heteroprotein. When a compound that acts positively upon an antitumor signal like TSA comes into contact with the cell, the expression of a
10 reporter gene existing downstream of the expression regulatory region in the second vector is induced through the activation of transcription or cancellation of the transcriptional repression of the reporter gene through the transcription activation region derived from the Sp3 protein in the fusion protein. Therefore, if this assay system using the reporter gene is employed, an efficient, Sp3-mediated screening of an anticancer
15 agent is possible by detecting the reporter activity in the cell after contacting the test sample and the cell.

Namely, the screening method of this invention includes the steps of (a) preparing a cell carrying (i) the first vector comprising, in an expressible manner, DNA encoding a fusion protein comprising a region having the transcriptional activation capacity of the
20 Sp3 protein and a region having the DNA binding capacity of a heteroprotein and (ii) the second vector that comprises a binding sequence of the heteroprotein, an expression regulatory sequence activated by the binding of the fusion protein, and a downstream reporter gene functionally bound to the regulatory sequence, (b) bringing a test sample into contact with the cell and measuring the reporter activity, and (c) selecting a
25 compound that elevates the reporter activity compared with a control test in which the test sample is not contacted with the cell.

The first vector used in the screening of this invention comprises, in an expressible manner, DNA encoding a fusion protein comprising a region having the transcriptional activation capacity of the Sp3 protein and a region having the DNA
30 binding capacity of a heteroprotein. Comprising DNA in an expressible manner means that the DNA encoding the fusion protein is connected to the expression regulatory

region (promoter or enhancer, for example) that ensures expression in the vector. For example, DNA encoding the fusion protein is inserted into the downstream of an appropriate promoter within the vector such as the CMV promoter, so that the vector can express the fusion protein in an appropriate host cell such as an animal cell or a yeast cell.

5 The region having transcriptional activation capacity of the Sp3 protein comprised in the fusion protein expressed by the first vector is not especially limited as long as it contains a region capable of transcriptional activation in response to a TSA stimulus. Desirably, such a region comprises at least a part of the transcription activation domain and lacks at least a part of the DNA binding domain. Although the screening of this
10 invention is possible even in the presence of the DNA binding region derived from Sp3, the presence of this region is not desirable because a fusion protein comprising this region can bind to various endogenous Sp1 binding sequences. In the case of human Sp3 protein, a desirable region comprises at least one of the two glutamine-rich regions (amino acids 10-123 and 223-358) and lacks at least a part of the Zinc finger region
15 (amino acids 495-517, 525-547, and 555-575) (Chris, K. et al., 1992, J. Biol. Chem., 12: 4251-4261). The species from which Sp3 protein derives is not limited. For example, Sp3 protein from humans, mammals, or other species can be used.

20 The region, specifically, amino acids 1-398, 81-398, 161-398, 1-320, 1-240, or 1-160 of human Sp3 protein as shown in figure 3 can be used appropriately for this invention, but it is not to be construed as being limited thereto.

25 The heteroprotein contained in the fusion protein expressed by the first vector is not specially limited as long as it can bind specifically to a specified DNA sequence. For example, the GAL4 protein, LexA protein (Gyuris, J. et al., 1993, Cell, 75: 791-803), tetracycline repressor protein (Tet R) (Manfred, G. et al., 1992, Proc. Natl. Acad. Sci.
USA, 89: 5547-5551) can be used as a heteroprotein, but the heteroprotein is not to be construed as being limited thereto. Partial peptides of these proteins can also be used as long as they bind specifically to a specified DNA sequence. The region having DNA binding capacity of the heteroprotein can be, for example, peptides comprising the DNA binding domain of GAL4 protein (for example, amino acids 1-94 or 1-147), the DNA
30 binding domain of LexA protein (for example, amino acids 1-202) (Erica, A. et al., 1992, Mol. Cell. Biol., 12: 3006-3014), and the DNA binding domain of tetracycline repressor

protein (Tet R) (Manfred, G. et al., 1992, Proc. Natl. Acad. Sci. USA, 89: 5547-5551), but the peptides are not to be construed as being limited thereto.

The second vector of this invention comprises a binding sequence of the heteroprotein, the expression regulatory sequence activated by the binding of the fusion protein, and the downstream reporter gene functionally bound to the regulatory sequence.

The binding sequence of the heteroprotein used for the construction of the second vector of this invention is not specially limited as long as the fusion protein expressed by the first expression vector can bind specifically to the binding sequence. For example, if the fusion protein comprises the GAL4 DNA binding region, the binding sequence can be, for example, "5'-cggasgacwgtcstccg-3'; s= c or g, w= a or t" (Marmorstein, R. et al., 1992, Nature 356: 408-414). If the fusion protein comprises the LexA DNA binding region, the binding sequence can be, for example, "5'-ctgtnnnnnnnnacag-3'; n= a, t, g, or c" (Erica, A. et al., 1992, Mol. Cell. Biol., 12: 3006-3014). If the fusion protein comprises the DNA binding domain of tetracycline repressor protein (Tet R), the binding sequence can be, for example, "5'-tccctatcagtgatagaga-3'" (Manfred, G. et al., 1992, Proc. Natl. Acad. Sci. USA, 89: 5547-5551).

It is desirable to use a binding sequence that is not recognized by endogenous proteins within the cell transfected by the vector. It is not desirable to use a sequence recognized by endogenous proteins because reporter activities generated in response to the actions of endogenous proteins may be detected.

To ensure that the downstream reporter gene is expressed when the fusion protein derived from the first vector binds to the binding sequence, a promoter sequence (such as the TATA sequence and Kozak sequence) can also be included in the second vector as an expression regulatory sequence in addition to the binding sequence.

When the DNA binding domain of GAL4 protein is used as the region having DNA binding capacity of the fusion protein derived from the first vector, the expression regulatory sequence used in the second vector can be, for example, the 5x GAL4 binding sequence, the E1B minimal promoter, and the DNA sequence containing TATA sequence.

In the second vector of the present invention, the reporter gene is functionally bound to the downstream of the expression regulatory sequence. The phrase

"functionally bound" indicates that the reporter gene is bound to the expression regulatory sequence so as to be expressed in response to the binding of the fusion protein derived from the first vector to the expression regulatory sequence.

Although the reporter gene used for this invention is not specially limited as long as its product is detectable, it is desirable to use a gene whose product can be detected without complicated manipulations such as Northern blotting analysis or Western blotting analysis. Suitable reporter genes are, for example, the luciferase gene, chloramphenicol acetyltransferase (CAT) gene, beta-galactosidase (β -Gal) gene, human growth hormone (hGH) gene, and secreted alkaline phosphatase (SEAP) gene.

The cell used for the screening of this invention is not specially limited. For example, a human cell or a mammalian cell, such as MG63 cell (a cell line derived from human osteosarcoma) genetically lacking p53 can be used. A yeast cell or a cell of a microorganism such as *Escherichia coli* can also be used. A method known to one skilled in the art can be used for gene manipulations for constructing vectors, for the introduction of the vectors into the cell, etc.

In the screening of this invention, a test sample is brought to contact with the cell into which the two vectors described above have been introduced, and the reporter activity is measured.

The test sample used for the screening can be, for example, a purified protein (including antibodies), gene library, products of a gene library, synthetic peptide library, cell extract, cell culture supernatant, synthetic low molecular compound library, natural extract, but it is not to be construed as being limited thereto. The test sample can be contacted with the cell by a method such as adding the test sample to cell culture medium or introducing the test sample into the cell (including the introduction of the gene) according to the kind of test sample used.

Reporter activity can be detected by a method known to one skilled in the art according to the kind of reporter gene used. For example, when luciferase gene is used as the reporter gene, the substrate for luciferase is added to the cell extract, and the amount of the light emitted by the enzymatic reaction is detected by a luminometer. When CAT gene is used as the reporter gene, the amount of CAT in the cell extract can be detected by the ELISA method using anti-CAT antibodies. When beta-galactosidase gene is used,

the substrate for beta-galactosidase is added to the cell extract, and the amount of the light emitted by the enzymatic reaction is detected by a luminometer. When human growth hormone (hGH) gene is used, the amount of hGH in cell culture can be detected by the ELISA method using anti-hGH antibodies. When secreted alkaline phosphatase (SEAP) gene is used as the reporter gene, the substrate for alkaline phosphatase is added to the cell culture, and the amount of light emitted by the enzymatic reaction can be detected by a luminometer.

If a significant increase in reporter activity is observed as a result of measuring reporter activity in comparison with a control test in which the test sample is not brought 10 into contact with the cell, the test sample used becomes a candidate for a compound that inhibits proliferation of a tumor.

In this invention, it was shown that the transcriptional activity mediated by Sp3 was promoted in the signal transduction from TSA involved in the tumor-suppressing effect. This fact shows that a compound that can enhance the transcriptional activity 15 mediated by Sp3 could have a tumor-suppressing effect. Thus, the present invention also relates to an anticancer agent comprising as an active ingredient a compound that enhances the transcriptional activity mediated by Sp3.

Such compounds that enhance Sp3 activity include various compounds having different sites of action. These compounds include, for example, those that act directly on Sp3 and promote its function, those that act upon molecules binding to Sp3 and promote function 20 of Sp3 indirectly, those that act upon a group of proteins involved in the reaction from the binding of Sp3 to DNA to the transcription, those that inhibit the interaction between Sp3 and HDAC, those that inhibit the activity of HDAC, and those that inhibit the function of Sp1. These compounds can be isolated by the above-mentioned screening of this 25 invention.

A compound of this invention which enhances the transcriptional activity mediated by Sp3 is thought to be applicable to a wide range of tumors. Because the induction of p21/WAF1/Cip1 expression mediated by Sp3 does not depend on p53, the compound is expected to be applicable especially to tumors having mutated or deleted 30 p53.

When a compound of this invention that enhances the transcriptional activity mediated by Sp3 is used as a pharmaceutical agent, it can be formulated by well-known pharmaceutical manufacturing methods. For example, the compound can be administered as a formulation mixed properly with a pharmaceutically acceptable carrier or vehicle, specifically with sterile water, physiological saline, plant oil, emulsifier agent, suspending agent, detergent, stabilizer, etc.

The compound can be administered to patients by, for example, transdermal, intranasal, transbronchial, intramuscular, intravenous, or oral administration depending on the properties of the compound.

Although dosage can vary depending on age, weight, and symptoms of the patient, the method of administration, and so on, one skilled in the art can suitably select an appropriate dosage. If the compound can be encoded by DNA, gene therapy is also possible by integrating the DNA into a vector for gene therapy. Although the dosage and method of administration can vary depending on the weight, age, symptoms, and such of a patient, one skilled in the art can suitably select an appropriate dosage and a administration method.

Brief Description of the Drawings

FIG. 1 is a photograph of a gel shift assay (EMSA) that shows the binding of Sp1 and Sp3 to the Sp1 binding sequence necessary for TSA dependent p21/WAF1/Cip1 promoter activation. EMSA was performed with nuclear extracts from both TSA-treated (lanes 5-9) and TSA-untreated (lanes 1-4) MG63 cells. The Sp1 binding sequence (positions -87 to -72 from the transcription start site), which is necessary for TSA dependent promoter activation, was used as a DNA probe. Supershift assay was carried out for each of the bands using anti-Sp1 antibodies (lanes 2, 4, 6, or 8) or anti-Sp3 antibodies (lanes 3, 4, 7, or 8). The positions of Sp1 and Sp3 bands are indicated on the left.

FIG. 2 shows TSA dependent transcriptional induction by Sp3. MG63 cells were cotransfected with 2.5 µg of either GAL4-Sp1 or GAL4-Sp3 plasmid and with 0.5 µg of pG5-luc reporter plasmid. At 24 hours posttransfection, TSA (500 ng/ml) was added, 24 hours later, the cells were lysed, and luciferase activity was measured. Transcriptional

induction by TSA is expressed as a ratio with respect to the TSA-untreated control value. Each experiment was carried out in triplicates and the data shown is a representative of five independent experiments.

FIG. 3 shows TSA dependent transcriptional induction mediated by the Sp3 glutamine-rich domain. Sequences of various GAL4-Sp3 deletion mutant proteins are indicated in the figure. The magnitudes of transcriptional induction by TSA upon expressing each of these proteins in the MG63 cells are indicated on the right. Transfection and TSA treatment were performed similarly to FIG. 2. Each experiment was carried out in triplicates and the data shown is a representative of three independent experiments.

FIG. 4 shows the repression of TSA dependent transcriptional induction of either the p21/WAF1/Cip1 promoter or the Sp1 promoter by dominant negative Sp3. MG63 cells were simultaneously transfected with 0, 1.25, 2.5, or 5.0 µg of pCMV-DNSp3 while adjusting the total amount of plasmids to 5.0 µg by adding pCMV3.1 control plasmid, and with 0.5 µg of reporter plasmid, pWWP (a), pWPdel-BstXI (b), Sp1-luc (c), or mtSp1-luc (d). Transfection and TSA treatment was performed similarly to FIG. 2. Each experiment was carried out in triplicates and the data shown is a representative of three independent experiments.

20 Best Mode for Carrying Out the Invention

Hereinafter, this invention will be described in detail using specific examples, however it is not to be construed as being limited thereto.

Example 1 Gel Shift Assay of the Sp1 Binding Sequence in the p21/WAF1/Cip1 25 Promoter

TSA induces transcription of p21/WAF1/Cip1 gene in a p53-independent manner through the Sp1 binding sequence, which exists in the promoter region of the p21/WAF1/Cip1 gene. Therefore, to elucidate the induction mechanism, the -87 to -72 bp region from the transcription start site, which is essential for transcriptional induction by TSA was used as a p21/WAF1/Cip1 probe and the binding protein was

analyzed by gel shift assay (electrophoretic mobility shift assay; EMSA) as described below.

(1-1) Cell Culture and Preparation of Nuclear Extracts

5 First, MG63 cells were incubated at 37°C in a humidified atmosphere of 5% CO₂ using DMEM medium (GIBCO BRL) containing 10% fetal calf serum (GIBCO BRL). Nuclear extracts of these cells were prepared from both TSA-treated and untreated cells, according to the method of Dignam et al. (Dignam, J. D. et al., (1983) Nucleic Acids Res. 11:1475-1489). First, cells cultured in a dish (100 mm) were incubated for 24 hours with
10 500 ng/ml TSA (Wako). This was then washed twice with cold PBS containing 0.5 mM 4-(2-aminoethyl)benzenesulfonyl fluoride HCl (p-ABSF) (Wako), the cells were scraped from the plate, and suspended in 10 mM Hepes/KOH buffer (pH7.9) containing 10 mM KCl, 1.5 mM MgCl₂, 0.5 mM DTT, 5 mM NaF, 5 mM NaVO₄, and 0.5 mM p-ABSF.
15 After placing on ice for 10 minutes, the cells were disrupted using a Dounce homogenizer. Upon centrifugation at 3,000 rpm for 10 minutes at 4°C, the nuclei were resuspended in 20 mM Hepes/KOH buffer (pH7.9) containing 400 mM NaCl, 1.5 mM MgCl₂, 25% glycerol, 0.1 mM EDTA, 1 mM DTT, 5 mM NaF, 5 mM NaVO₄, and 0.5 mM p-ABSF and mixed at 4°C for 60 minutes to extract the nuclear components.
20 This extract was centrifuged at 35,000 rpm for 30 minutes at 4°C and the supernatant was recovered as nuclear extracts. The obtained nuclear extracts were dialyzed against 20 mM Hepes/KOH buffer (pH7.9) containing 400 mM KCl, 20% glycerol, 0.1 mM EDTA, 1 mM DTT, 5 mM NaF, 5 mM NaVO₄, and 0.5 mM p-ABSF, and were stored at -80°C.

25 (1-2) Gel Shift Assay (EMSA)

Next, based on the TSA-dependent promoter sequence (5'-CGGGTCCCGCCTCCTT-3' / SEQ ID NO: 1) located -87 to -72 bp from the transcription start site of the p21/WAF1/Cip1 gene, oligonucleotides (5'-AGCTCGGGTCCCGCCTCCTT-3' / SEQ ID NO: 2, and
30 5'-TCGAAAGGAGGCAGGGACCCG-3' / SEQ ID NO: 3) were synthesized. Upon annealing, the DNAs were labeled using [α -³³P] dCTP and Klenow Fragment

(TAKARA), and these were used as DNA probes. After incubation of the abovementioned nuclear extract (8 µg) in 20 µl of reaction solution (8 mM Tris/HCl (pH7.9), 24 mM Hepes/KCl (pH7.9), 120 mM KCl, 24% glycerol, 2 mM EDTA, 2 mM DTT, 1 mg poly (dI-dC) (Pharmacia)) for 5 minutes, the ³³P-labeled DNA probe (specific activity of 50,000 cpm/µl) was added and the binding reaction was allowed to proceed for 20 minutes. In the antibody supershift assay experiment, which will be described later, 2 µg of anti-Sp1 antibody or 1 µg of anti-Sp3 antibody (Santa Cruz, sc-59X and sc-644X) was further added and incubated for 20 minutes. The reaction solution was resolved by electrophoresis on a 6% acrylamide gel and the proteins that bind to the p21/WAF1/Cip1 probe were detected using BAS 2000 (Fujix).

10 (1-3) Result

When the nuclear extract prepared from TSA-treated and untreated MG63 cells were reacted with the p21/WAF1/Cip1 probe, and the gel shift assay described above was carried out, two specific bands were detected (FIG. 1, 1 and 5). Next, when the reactivity of each of the supershifted bands was observed by the abovementioned method using anti-Sp1 or anti-Sp3 antibody, a portion of the upper band shifted in the presence of the anti-Sp1 antibody, two bands including a portion of the upper band and the lower band shifted in the presence of anti-Sp3 antibody, and all bands shifted when both anti-Sp1 antibody and anti-Sp3 antibody were added (FIG. 1). The two Sp3 bands are thought to originate from large (97 kDa) and small (60 kDa and 65 kDa) Sp3 proteins, respectively (Gustav, H. et al., (1994) EMBO J. 13: 3843-3851; Addanki, P. B. et al., (1997) Nucleic Acids Res. 25: 2012-2019). Therefore, Sp1 and Sp3 present in the nuclear extract of MG63 cells were actually shown to bind to the Sp1 binding region of p21/WAF1/Cip1, and this suggested that Sp1 and Sp3 were involved in TSA dependent transcriptional induction. These results are consistent with previous reports made by the inventors (Nakano, K. et al., (1997) J. Biol. Chem. 272: 22199-22206) and by other groups (Datto, M. B. et al., (1995) J. Biol. Chem. 270: 28623-28628; Adnane, J. et al., (1998) Mol. Cell. Biol. 18: 6962-6970). However, a difference in the amount of DNA bound by Sp1 and Sp3 due to the presence or absence of TSA treatment could not be observed (FIG. 1). Therefore, TSA dependent transcriptional induction seemed to take place through

mechanisms other than differences in the amount of Sp1 or Sp3 expressed, or differences in their ability to bind to DNA. This is also consistent with the inventors' report using sodium butyrate, an HDAC inhibitor (Nakano, K. et al., (1997) J. Biol. Chem. 272: 22199-22206) and with the report by Datto et al. observing TGF- β -dependent transcriptional induction (Datto, M. B. et al., (1995) J. Biol. Chem. 270: 28623-28628), but is inconsistent with the report by Adnane et al. using geranyl geranyl-transferase I inhibitor (Adnane, J. et al., (1998) Mol. Cell. Biol. 18: 6962-6970).

Example 2 Reporter Assay Using the GAL4 Binding Sequence

TSA causes transcriptional induction through the Sp1 binding sequence of the p21/WAF1/Cip1 promoter, and similarly, it can cause transcriptional induction through the 3x Sp1 consensus binding sequence inserted into the SV40 promoter (Sowa, Y. et al., (1997) Biochem. Biophys. Res. Comm. 241:142-150). Consequently, to determine whether Sp1 or Sp3 that bind to this Sp1 binding sequence is actually involved in transcriptional induction caused by TSA treatment, a reporter assay system using the GAL4 binding sequence was examined. Namely, when trying to observe effects of Sp1 or Sp3 by forced expression, endogenous effects of Sp1 or Sp3 will be detected if the Sp1 binding sequence is used as a promoter for the reporter gene. Therefore, forced expression of a fusion protein formed between the DNA binding domain of bacterial GAL4 protein and Sp1 or Sp3 allowed analysis of whether GAL4 binding sequence-dependent transcriptional activity is induced by TSA or whether Sp1 or Sp3 regulates this induction.

(2-1) Expression Plasmid and Reporter Plasmid

To express GAL4 proteins that have Sp1 (amino acids 83-778), full-length Sp3 (amino acids 1-653), transcriptional activation domain-deleted Sp1 (amino acids 592-778) (DNSp1), or transcriptional activation domain-deleted Sp3 (amino acids 399-653) (DNSp3) attached to the C-terminal end of their DNA binding domain, each of these genes were inserted into a pM vector (Clontech) possessing a GAL4 binding domain. This yielded pM-Sp1, pM-Sp3, pM-DNSp1, and pM-DNSp3, respectively. Each of the Sp1 and Sp3 genes was amplified by PCR. Specifically, pM-Sp1 production employed

Sp1-S (5'-acaggtgagcttga-3' / SEQ ID NO: 4) and Sp1-AS (5'-tcagaagccattgcc-3' / SEQ ID NO: 5) as primers and used pPacSp1 as template for amplification (Kadonaga, J. T. et al., (1987) Cell 51: 1079-1090). pM-DNSp1 production employed DNSp1-S (5'-ccaaaaagaagagaaaggtaaccggcgg-3' / SEQ ID NO: 6) and DNSp1-AS (5'-gaagcatgcacctgc-3' / SEQ ID NO: 7) as primers and used pM-Sp1 as template for amplification (Kadonaga, J. T. et al., (1987) Cell 51: 1079-1090). pM-Sp3 production employed Sp3-18F (5'-cgggatccattccaagtgtctgtct-3' / SEQ ID NO: 8) and Sp3-2R (5'-ataggatccttactccattgtctcatttcc-3' / SEQ ID NO: 9) as primers and used Marathon-Ready cDNA (Human Fetal Liver) (Clontech, Cat. #7403-1) as template for amplification (Chris, K. et al., (1992) J. Biol. Chem. 12: 4251-4261). pM-DNSp3 production employed Sp3-11F (5'-cgggatccaactctataggattctgtct-3' / SEQ ID NO: 10) and Sp3-2R (SEQ ID NO: 9) as primers and used pM-Sp3 as template for amplification (Chris, K. et al., (1992) J. Biol. Chem. 12: 4251-4261). All PCRs were carried out by performing 30 cycles of 94°C for 1 minute, 55°C for 30 seconds, and 72°C for 30 seconds. The resulting PCR amplified product was inserted into a pM vector and the nucleotide sequence was confirmed using a DNA sequencer, ABI PRISM 355 (Applied Bio System). As a control for the transfection test, pM that only expresses the GAL4 DNA binding domain was employed. The reporter plasmid (pG5-luc) used to indicate the dependence of transcriptional activation, on GAL4 was pGL3-Basic Vector (Promega), which carried the 5x GAL4 binding sequence, E1B minimum promoter, and TATA sequence, upstream of the luciferase gene.

(2-2) Transfection Assay

The expression vector described above encoding various Sp1 or Sp3 GAL4 fusion proteins and the abovementioned vector carrying a luciferase reporter gene downstream of the consensus 5x GAL4 binding sequence were cotransfected into MG63 cells using SuperFect following the method by QIAGEN. Namely, cells were seeded at a density of 0.8x 10⁵ cells/well in a 12-well plate. After 24 hours, a pre-mixed reaction solution containing 0.5 µg of reporter plasmid, 2.5 µg of expression vector, and SuperFect were added to the MG63 cells and the mixture was reacted for 2 hours. Subsequently, the cells were cultured for 24 hours under normal culture conditions, cultured for another 24 hours

with or without (control) 500 ng/ml of TSA, and then, the cells were lysed. Using luciferase substrate (Promega), luciferase activity of the cell lysates was measured using LB-96P (Berthold). The measured values were normalized and were expressed as activity per amount of protein. Transcriptional induction due to TSA treatment was 5 calculated as a ratio with respect to the TSA-untreated control value (activation amplification by TSA).

(2-3) Result

Although GAL4-Sp1 and GAL4-Sp3 both showed transcriptional activity even 10 without TSA treatment, this seemed to be mediated through the transcriptional activation domain present within Sp1 and Sp3 themselves. When treated with TSA, cells expressing GAL4-Sp3 showed strong transcriptional induction of the luciferase gene, whereas activity in the cells expressing GAL4-Sp1 was similar in magnitude to that seen in the control using GAL4 (FIG. 2). Furthermore, when a similar study was carried out 15 with the fusion protein made from the N-terminal end transcriptional activation domain-deleted Sp1 or Sp3, and the GAL4 DNA binding domain, described above, GAL4-DNSp3 no longer showed TSA dependent transcriptional induction (FIG. 2). These results suggested that transcriptional induction of the p21/WAF1/Cip1 gene by TSA treatment occurs through the transcriptional activation domain of Sp3, bound to the Sp1 20 binding sequence of the promoter.

Example 3 Identification of the TSA Responsive Domain of Sp3

Next, reporter assay was performed using various Sp3 deletion mutants fused to the GAL4 DNA binding domain in order to identify the TSA responsive region of Sp3. 25 First, pM-Sp3 (1-398), pM-Sp3 (81-398), pM-Sp3 (161-398), pM-Sp3 (241-398), pM-Sp3 (1-80), pM-Sp3 (1-160), pM-Sp3 (1-240), and pM-Sp3 (1-320) were prepared. They respectively carry regions corresponding to the indicated amino acid numbers. Each of the Sp1 and Sp3 genes were amplified by PCR, inserted into a pM vector, and the nucleotide sequences were confirmed using a DNA sequencer, ABI PRISM 355 (Applied 30 Bio System). The primer sequences used for PCR amplification are shown in Table 1.

PCR was carried out using pM-Sp3 as the template, performing 25 cycles of 98°C for 15 seconds, 65°C for 2 seconds and 74°C for 30 seconds.

Table 1

	Plasmid	Primer
5	pM-Sp3(1-398)	Sp3-18F (5'-cgggatccattccaagtgcgtct-3' / SEQ ID NO: 8) Sp3(1194-1177)AS + BamHI (5'-gcggatcccactgttaactgttttag-3' / SEQ ID NO: 11)
10	pM-Sp3 (81-398)	Sp3(241-260) S + BamHI (5'-cgggatccggcttaatcaaaccctact-3' / SEQ ID NO: 12) Sp3(1194-1177)AS + BamHI (SEQ ID NO: 11)
15	pM-Sp3 (161-398)	Sp3(481-500) S + BamHI (5'-cgggatccggcattaatgccgacggaca-3' / SEQ ID NO: 13) Sp3(1194-1177)AS + BamHI (SEQ ID NO: 11)
20	pM-Sp3 (241-398)	Sp3(721-740) S + BamHI; (5'-cgggatcccaggaaatttatccagtc-3' / SEQ ID NO: 14) Sp3(1194-1177)AS + BamHI (SEQ ID NO: 11)
25	pM-Sp3 (1-80)	Sp3-18F (SEQ ID NO: 8) Sp3(240-221)AS + BamHI (5'-cgggatccaggaatgtatctgaatttgac-3' / SEQ ID NO: 15)
30	pM-Sp3 (1-160)	Sp3-18F (SEQ ID NO: 8) Sp3(480-461)AS + BamHI (5'-cgggatcctgcagtcaattgtctgagaac-3' / SEQ ID NO: 16)

PCT/US03/03933 03/03934 03/03935 03/03936

pM-Sp3 (1-240)
Sp3-18F (SEQ ID NO: 8)
Sp3(720-701)AS + BamHI
(5'-cgggatccaagatctagaagaatgaacct-3' SEQ ID NO: 17)

5 pM-Sp3 (1-320)
Sp3-18F (SEQ ID NO: 8)
Sp3(960-941)AS + BamHI
(5'-cgggatccaaagggtccaggattcagct-3' SEQ ID NO: 18)

10

As a control for the transfection test, pM expressing only the GAL4 DNA binding domain was used. The reporter plasmid (pG5-luc) used as an index for GAL4 dependent transcriptional activation was the abovementioned pGL3-Basic Vector (Promega).

15 Transfection using these genes followed the same method as described above, and the occurrence of transcriptional induction due to TSA treatment in these mutants was monitored. Consequently, TSA dependent transcriptional induction occurred with GAL4-Sp3 (1-398) that lacks the Sp3 DNA binding domain (FIG. 3), and this induction was in fact stronger than with GAL4-Sp3 (FIG. 3). This result correlated with the aforementioned result (Example 2) where deletion of the N-terminal end transcriptional 20 activation domain caused the termination of transcriptional induction due to TSA treatment. This also suggested a correlation with the report describing that of the two glutamine-rich domains in Sp3, the repressive domain existing between the C-terminal domain and the DNA binding domain represses the transcriptional activation of Sp3 (Dennig, J. et al., (1996) EMBO J. 15: 5659-5667; Majello B et al., (1997) J. Biol. Chem. 25 272: 4021-4026).

25 As FIG. 3 shows, when deletions were made from the N-terminal end or from the C-terminal end of Sp3 (1-398), induction due to TSA treatment disappeared with GAL4-Sp3 (241-398) and with GAL4-Sp3 (1-80). From these results, Sp3 (81-160) seemed important for transcriptional induction due to TSA treatment. However, GAL4-Sp3 (81-30 160) alone showed almost no activity. Since both GAL4-Sp3 (241-398) and GAL4-Sp3 (1-80) lack a complete glutamine-rich domain, transcriptional induction by TSA seems to

require the presence of at least one of the two glutamine-rich domains in the Sp3 transcriptional activation domain. The 80-160 region of Sp3 may contain part of an important region for TSA mediated transcriptional induction.

5 Example 4 Dominant Negative Sp3

Moreover, to determine whether Sp3 actually mediates transcriptional induction by TSA through the Sp1 binding sequence of p21/WAF1/Cip1, the transcriptional activation domain was deleted, and a Sp3 mutant (DNSp3) (amino acid 399-653) which only has the DNA binding domain was integrated into pCMV3.1-His-C (Invitrogen) to produce pCMV-DNSp3. pCMV3.1 was used as a control. The reporter plasmids used were pWWP and pWPdel-BstXI, which have the previously reported p21/WAF1/Cip1 promoter and the TSA dependent p21/WAF1/Cip1 minimum promoter inserted upstream of the luciferase gene, respectively, and Sp1-luc and mtSp1-luc, which have 3x Sp1 binding sequence and mutant 3x Sp1 binding sequence inserted upstream of the luciferase gene, respectively (Nakano, K. et al., (1997) J. Biol. Chem. 272: 22199-22206; Sowa, Y. et al., (1997) Biochem. Biophys. Res. Comm. 241: 142-150).

Through forced expression of these genes by transfection using the same method as described above, the inventors examined whether these genes function in a dominant negative fashion towards transcriptional induction by TSA. Consequently, transcriptional induction of p21/WAF1/Cip1 by TSA was remarkably repressed by DNSp3 and this was confirmed by pWPdel-BstXI as well, which has the smallest unit of TSA dependent p21/WAF1/Cip1 promoter that carries the Sp1 binding sequence (+16 to -101 from the transcription start site) (FIG. 4a, b). Similarly, TSA dependent transcriptional induction driven by the consensus Sp1 binding sequence showed marked repression (FIG. 4c). When the mutated Sp1 binding sequence was used, transcriptional induction by TSA did not take place, and the effect of DNSp3 was absent as well (FIG. 4d). In either promoter, DNSp3 did not show repression towards TSA-untreated basic transcriptional activity. These results revealed the importance of the Sp3 transcriptional activation domain in TSA dependent p21/WAF1/Cip1 transcriptional induction. It is assumed that in the absence of TSA treatment, Sp3 only has extremely weak transcriptional factor activity,

however, in the presence of TSA treatment, a molecule acetylated by repression of HDAC is recognized and subsequently strong transcriptional activity is expressed.

Recently, as a new approach against cancer, transcription-regulating chemotherapy and transcription-regulating chemoprevention were proposed (Sakai, T., 5 (1996) Jpn. J. Hyg. 50: 1036-1046). The strategy is to induce the transcription of cell-proliferation suppressive p53 target genes, thereby exhibiting anticancer activity. However, as a target for transcriptional induction, the finding that p53 is mutated in many human tumor cells (Sakai, T., (1996) Jpn. J. Hyg. 50: 1036-1046; Vogelstein, B. and Kinzler, K. W., (1992) Cell 70: 523-526) is a drawback. In contrast, almost no mutation 10 has been reported in human cancer cells for p21/WAF1/Cip1, which is one of the target genes of p53 and has cell-cycle suppressing activity (Chedid, M et al., (1994) Oncogene 9: 3021-3024; Li, Y. J. et al., (1995) Oncogene 10: 599-601). Therefore, anticancer activity can be expected through transcriptional induction of p21/WAF1/Cip1. This invention revealed that a pathway exists for p53 independent p21/WAF1/Cip1 15 transcriptional induction mediated by histone acetylation, and suggests that transcription-regulating chemotherapy or transcription-regulating chemoprevention of cancer is possible even when p53 is mutated. HDAC inhibitors are regarded as possible drugs, and in reality, sodium phenylbutyrate, an HDAC inhibitor previously used for the treatment of thalassemia and hyperammonemic states, in combination with all-trans retinoic acid 20 was shown to induce complete remission of all-trans-retinoic acid resistant acute promyelocytic leukemia (Warrel, R. P., Jr. et al., (1998) J. Natl. Cancer Inst. 90: 1621-1625). These results suggest HDAC as one of the possible target molecules for cancer therapy.

25 Industrial Applicability

This invention showed that Sp3, which regulates HDAC, could be a new target molecule for cancer therapy. This invention also provided an efficient Sp3-targeted method for screening antitumor agents. Compounds isolated by the screening method of this invention are expected to be applied in novel transcription-regulating chemotherapy 30 and chemoprevention against cancer.

CLAIMS

1. A method for screening an anticancer agent, comprising the steps of:
 - (a) preparing a cell carrying (i) a first vector comprising, in an expressible manner, DNA encoding a fusion protein comprising a region having the transcriptional activation capacity of the Sp3 protein and a region having the DNA binding capacity of a heteroprotein, and, (ii) a second vector comprising a binding sequence of the heteroprotein, an expression regulatory sequence activated by the binding of the fusion protein, and a downstream reporter gene functionally bound to the regulatory sequence,
 - 10 (b) contacting a test sample with the cell and measuring reporter activity, and,
 - (c) selecting a compound that elevates reporter activity in comparison with a control test in which the test sample is not contacted with the cell.
2. The method of claim 1, wherein the heteroprotein is the GAL4 protein,
15 LexA protein, or tetracycline repressor protein.
3. The method of claim 1 or 2, wherein the reporter gene is encoding
luciferase, chloramphenicol acetyltransferase, beta-galactosidase, human growth
hormone, or secreted alkaline phosphatase.
20
4. An anticancer agent comprising a compound that enhances the
transcriptional activity mediated by Sp3 as an active ingredient.
5. The anticancer agent of claim 4, wherein the agent can be isolated by a
25 method of any one of claims 1 to 3.

ABSTRACT

By analyzing the mechanism for inducing a histone deacetylase inhibitor (Trichostatin A)-mediated expression of cyclin-CDK inhibitory factor having a proliferation suppressing effect (tumor-suppressing effect), it was revealed that the binding of Sp3 to the Sp1 binding sequence within a promoter is important in the expression of the above factor. Thus, a novel antitumor agent can be developed by screening a pharmaceutical agent capable of elevating Sp3 activity.

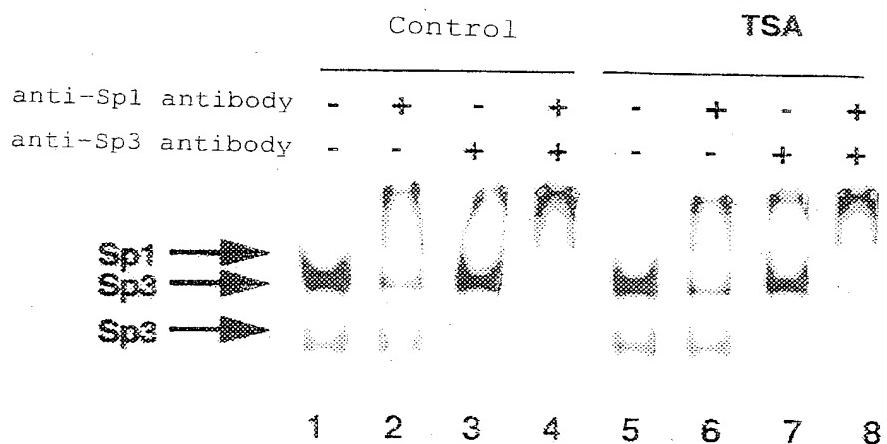
10

09/937162

1000 μl of cell lysate was loaded onto each lane.

1 / 4

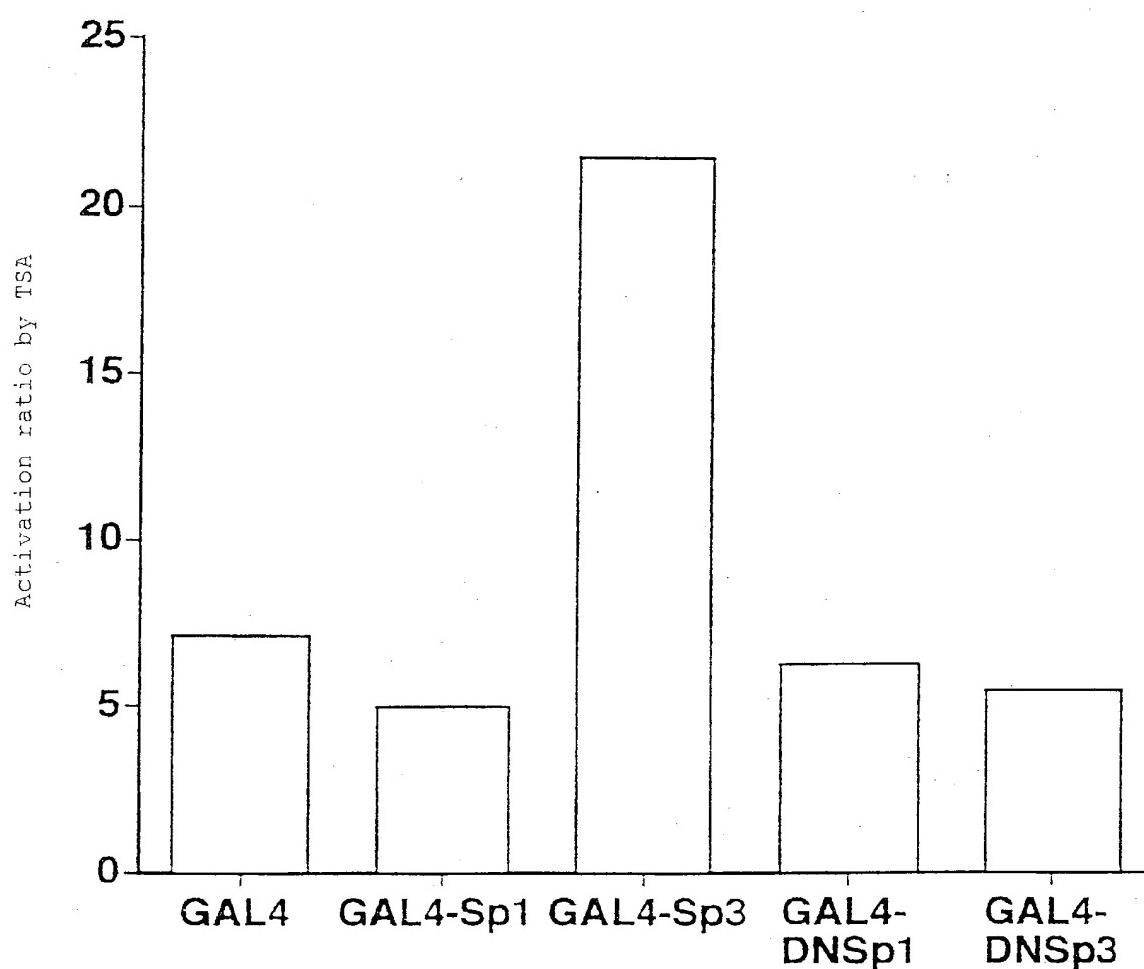
Figure 1



09/937162

2 / 4

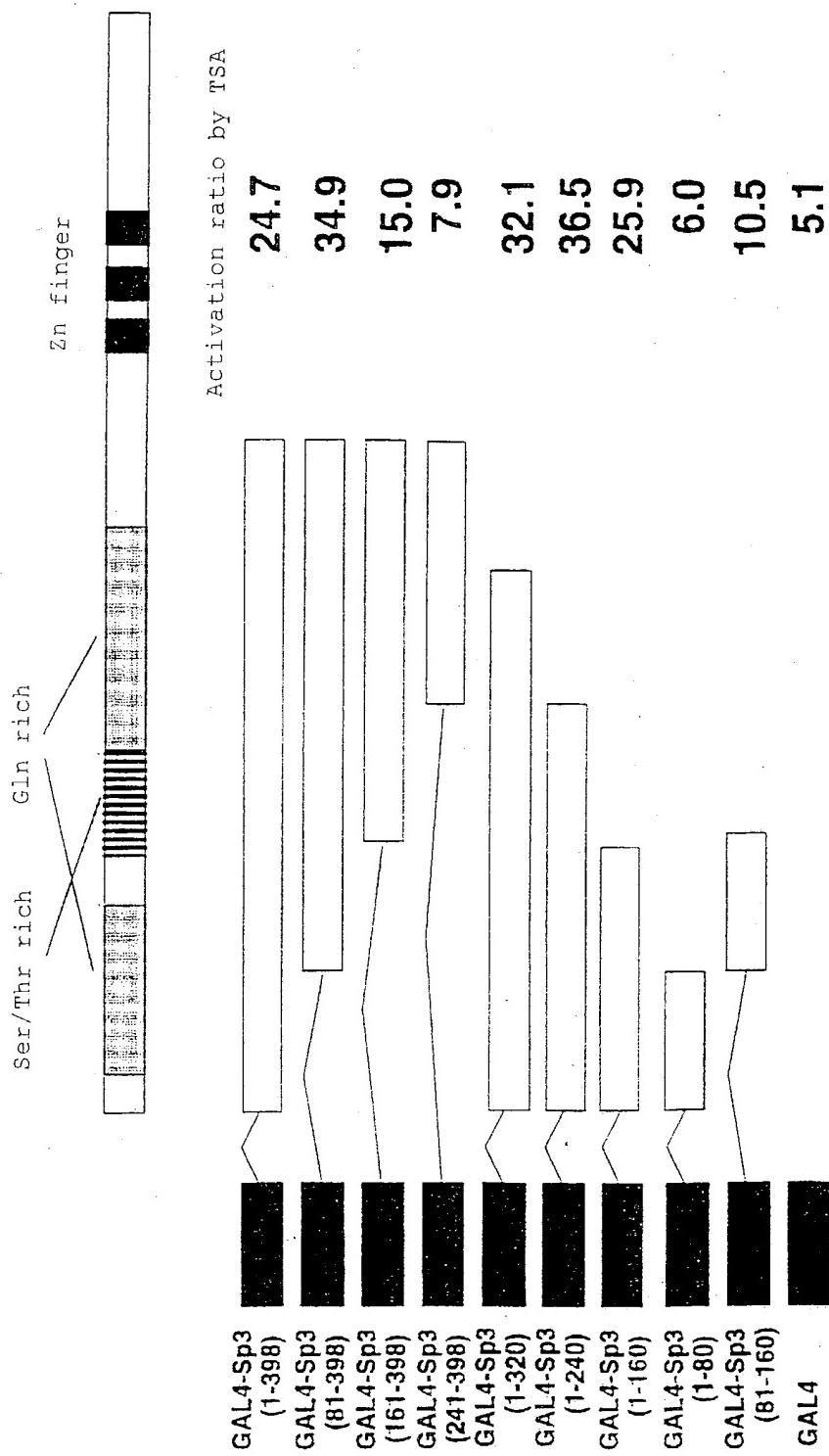
Figure 2



09/937162

CO / 4

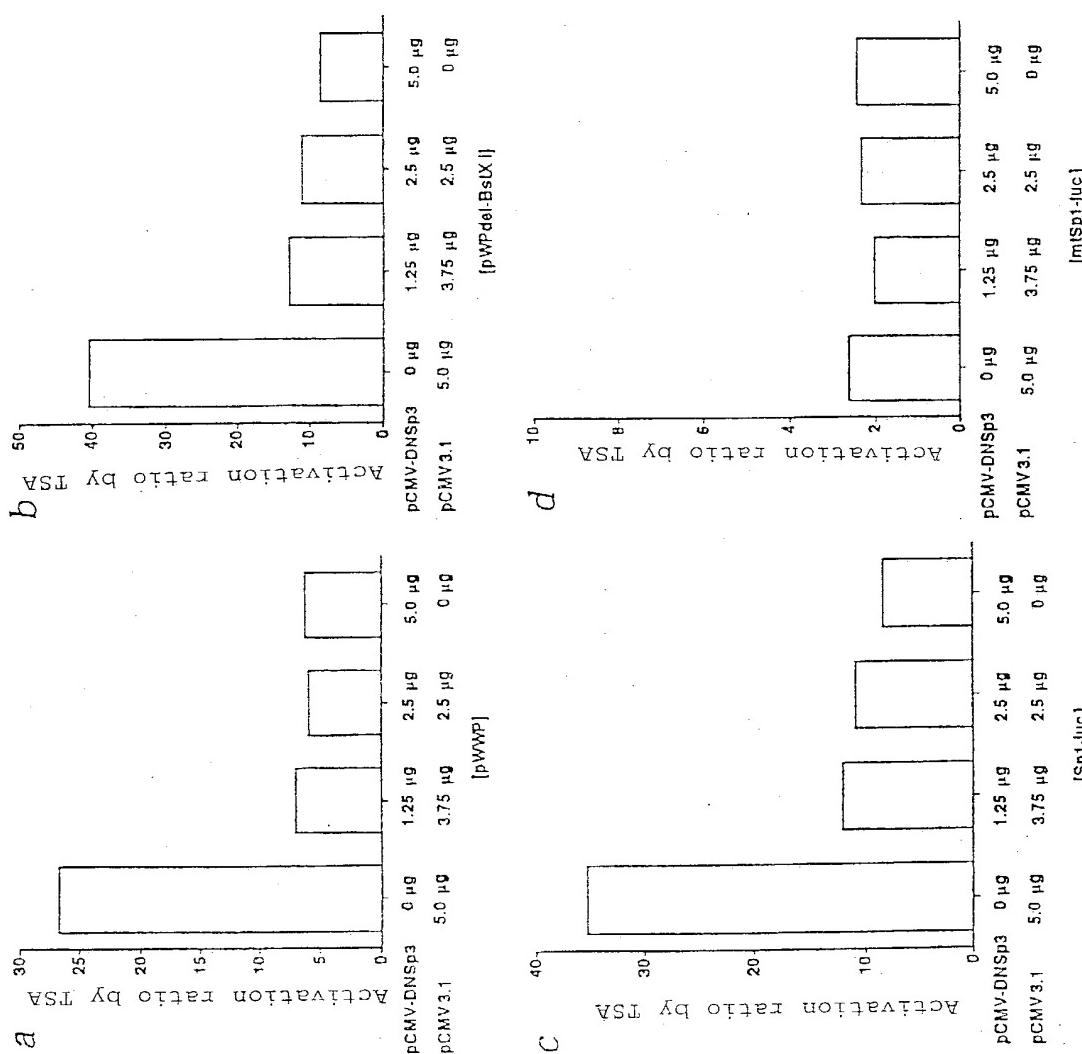
Figure 3



09/937162

4 / 4

Figure 4



COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled METHOD FOR SCREENING ANTICANCER AGENT, the specification of which:

- is attached hereto.
 was filed on _____ as Application Serial No. _____ and was amended on _____
 was described and claimed in PCT International Application No. PCT/JP00/01778 filed on March 23, 2000 and as amended under PCT Article 19 on _____

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information I know to be material to patentability in accordance with Title 37, Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate or of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

Country	Application No.	Filing Date	Priority Claimed
Japan	11/77350	March 23, 1999	<input type="checkbox"/> Yes <input type="checkbox"/> No
PCT	PCT/JP00/01778	March 23, 2000	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No

I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

Janis K. Fraser, Ph.D., J.D., Reg. No. 34,819
Timothy A. French, Reg. No. 30,175
Ralph A. Mittelberger, Reg. No. 33,195

John W. Freeman, Reg. No. 29,066
Anita L. Meiklejohn, Reg. No. 35,283

5

Address all telephone calls to JANIS K. FRASER, PH.D., J.D. at telephone number (617) 542-5070.

Address all correspondence to JANIS K. FRASER, PH.D., J.D. at:

FISH & RICHARDSON P.C.
225 Franklin Street
Boston, Massachusetts 02110-2804

Combined Declaration and Power of Attorney

Page 2 of 2 Pages

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

1-50

Full Name of Inventor: YOSHIHIRO SOWA

Inventor's Signature:

Yoshihiro Sowa

Date: December 26, 2001

Residence Address:

Kyoto, Japan JPX

Citizenship:

Japan

Post Office Address:

201 Yanagikoji, 335-3, Yanagimachi
Higashinakasujidori Hanayacho sagaru
Shimogyo-ku, Kyoto-shi
Kyoto 600-8344 Japan

2-50

Full Name of Inventor: TETSURO ORITA

Inventor's Signature:

Tetsuro Orita

Date: December 20, 2001

Residence Address:

Ibaraki, Japan JPX

Citizenship:

Japan

Post Office Address:

c/o Tsukuba Research Laboratory
Chugai Seiyaku Kabushiki Kaisha
153-2, Nagai, Niihari-mura, Niihari-gun
Ibaraki 300-4101 Japan